Low Fluid Shear Culture of *Staphylococcus aureus* Represses *hfq* Expression and Induces an Attachment-Independent Biofilm Phenotype

Background: The opportunistic pathogen, *Staphylococcus aureus*, experiences fluctuations in fluid shear during infection and colonization of a human host. Colonization frequently occurs at mucus membrane sites such as in the gastrointestinal tract where the bacterium may experience low levels of fluid shear. The response of *S. aureus* to low fluid shear remains unclear. **Methods:** *S. aureus* was cultured to stationary phase using Rotating-Wall Vessel (RWV) bioreactors which produce a physiologically relevant low fluid shear environment. The bacterial aggregates that developed in the RWV were evaluated by electron microscopy as well as for antibiotic resistance and other virulence-associated stressors. Genetic expression profiles for the low-shear cultured *S. aureus* were determined by microarray analysis and quantitative real-time PCR. **Results:** Planktonic *S. aureus* cultures in the low-shear environment formed aggregates completely encased in high amounts of extracellular polymeric substances. In addition, these aggregates demonstrated increased antibiotic resistance indicating attachment-independent biofilm formation. Carotenoid production in the low-shear cultured *S. aureus* was significantly decreased, and these cultures displayed an increased susceptibility to oxidative stress and killing by whole blood. The *hfq* gene, associated with low-shear growth in Gram negative organisms, was also found to be down-regulated in *S. aureus*. **Conclusions:** Collectively, this data suggests that *S. aureus* decreases virulence characteristics in favor of a biofilm-dwelling colonization phenotype in response to a low fluid shear environment. Furthermore, the identification of an Hfq response to low-shear culture in *S. aureus*, in addition to the previously reported responses in Gram negative organisms, strongly suggests an evolutionarily conserved response to mechanical stimuli among structurally diverse prokaryotes.